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RAW SEQUENCE LISTING DATE: 01/15/2002
PATENT APPLICATION: US/09/966,755 TIME: 17:36:26

Input Set : N:\Crf3\RULE60\09966755.raw
Output Set: N:\CRF3\01152002\I966755.raw

<110> APPLICANT: Andrew, David P.
Zabel, Brian A.
Ponath, Paul D.
<120> TITLE OF INVENTION: ANTI-GPR-9-6 ANTIBODIES AND METHODS OF IDENTIFYING AGENTS WHICH MODULATE GPR-9-6 FUNCTION
<130> FILE REFERENCE: LKS98-16
<140> CURRENT APPLICATION NUMBER: 09/966,755
<141> CURRENT FILING DATE: 2001-09-28
<150> PRIOR APPLICATION NUMBER: US/09/266,464
<151> PRIOR FILING DATE: 1999-03-11
<160> NUMBER OF SEQ ID NOS: 7
<170> SOFTWARE: FastSEQ for Windows Version 3.0

ENTERED

<210> SEQ ID NO: 1
<211> LENGTH: 2577
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (58)...(1131)
<400> SEQUENCE: 1

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                                                                  Met
                                                                   1

gct gat gac tat ggc tct gaa tcc aca tct tcc atg gaa gac tac gtt      108
Ala Asp Asp Tyr Gly Ser Glu Ser Thr Ser Ser Met Glu Asp Tyr Val
  5                  10                  15

aac ttc aac ttc act gac ttc tac tgt gag aaa aac aat gtc agg cag      156
Asn Phe Asn Phe Thr Asp Phe Tyr Cys Glu Lys Asn Asn Val Arg Gln
            20                  25                  30

ttt gcg agc cat ttc ctc cca ccc ttg tac tgg ctc gtg ttc atc gtg      204
Phe Ala Ser His Phe Leu Pro Pro Leu Tyr Trp Leu Val Phe Ile Val
        35                  40                  45

ggt gcc ttg ggc aac agt ctt gtt atc ctt gtc tac tgg tac tgc aca      252
Gly Ala Leu Gly Asn Ser Leu Val Ile Leu Val Tyr Trp Tyr Cys Thr
    50                  55                  60                  65

aga gtg aag acc atg acc gac atg ttc ctt ttg aat ttg gca att gct      300
Arg Val Lys Thr Met Thr Asp Met Phe Leu Leu Asn Leu Ala Ile Ala
                70                  75                  80

gac ctc ctc ttt ctt gtc act ctt ccc ttc tgg gcc att gct gct gct      348
Asp Leu Leu Phe Leu Val Thr Leu Pro Phe Trp Ala Ile Ala Ala Ala
            85                  90                  95

gac cag tgg aag ttc cag acc ttc atg tgc aag gtg gtc aac agc atg      396
Asp Gln Trp Lys Phe Gln Thr Phe Met Cys Lys Val Val Asn Ser Met
        100                 105                 110

tac aag atg aac ttc tac agc tgt gtg ttg ctg atc atg tgc atc agc      444
Tyr Lys Met Asn Phe Tyr Ser Cys Val Leu Leu Ile Met Cys Ile Ser
    115                 120                 125
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52   gtg gac agg tac att gcc att gcc cag gcc atg aga gca cat act tgg      492
53   Val Asp Arg Tyr Ile Ala Ile Ala Gln Ala Met Arg Ala His Thr Trp
54   130                 135                 140                 145
55   agg gag aaa agg ctt ttg tac agc aaa atg gtt tgc ttt acc atc tgg      540
56   Arg Glu Lys Arg Leu Leu Tyr Ser Lys Met Val Cys Phe Thr Ile Trp
57                   150                 155                 160
58   gta ttg gca gct gct ctc tgc atc cca gaa atc tta tac agc caa atc      588
59   Val Leu Ala Ala Ala Leu Cys Ile Pro Glu Ile Leu Tyr Ser Gln Ile
60               165                 170                 175
61   aag gag gaa tcc ggc att gct atc tgc acc atg gtt tac cct agc gat      636
62   Lys Glu Glu Ser Gly Ile Ala Ile Cys Thr Met Val Tyr Pro Ser Asp
63           180                 185                 190
64   gag agc acc aaa ctg aag tca gct gtc ttg acc ctg aag gtc att ctg      684
65   Glu Ser Thr Lys Leu Lys Ser Ala Val Leu Thr Leu Lys Val Ile Leu
66       195                 200                 205
67   ggg ttc ttc ctt ccc ttc gtg gtc atg gct tgc tgc tat acc atc atc      732
68   Gly Phe Phe Leu Pro Phe Val Val Met Ala Cys Cys Tyr Thr Ile Ile
69   210                 215                 220                 225
70   att cac acc ctg ata caa gcc aag aag tct tcc aag cac aaa gcc cta      780
71   Ile His Thr Leu Ile Gln Ala Lys Lys Ser Ser Lys His Lys Ala Leu
72                   230                 235                 240
73   aaa gtg acc atc act gtc ctg acc gtc ttt gtc ttg tct cag ttt ccc      828
74   Lys Val Thr Ile Thr Val Leu Thr Val Phe Val Leu Ser Gln Phe Pro
75               245                 250                 255
76   tac aac tgc att ttg ttg gtg cag acc att gac gcc tat gcc atg ttc      876
77   Tyr Asn Cys Ile Leu Leu Val Gln Thr Ile Asp Ala Tyr Ala Met Phe
78           260                 265                 270
79   atc tcc aac tgt gcc gtt tcc acc aac att gac atc tgc ttc cag gtc      924
80   Ile Ser Asn Cys Ala Val Ser Thr Asn Ile Asp Ile Cys Phe Gln Val
81       275                 280                 285
82   acc cag acc atc gcc ttc ttc cac agt tgc ctg aac cct gtt ctc tat      972
83   Thr Gln Thr Ile Ala Phe Phe His Ser Cys Leu Asn Pro Val Leu Tyr
84   290                 295                 300                 305
85   gtt ttt gtg ggt gag aga ttc cgc cgg gat ctc gtg aaa acc ctg aag     1020
86   Val Phe Val Gly Glu Arg Phe Arg Arg Asp Leu Val Lys Thr Leu Lys
87                   310                 315                 320
88   aac ttg ggt tgc atc agc cag gcc cag tgg gtt tca ttt aca agg aga     1068
89   Asn Leu Gly Cys Ile Ser Gln Ala Gln Trp Val Ser Phe Thr Arg Arg
90               325                 330                 335
91   gag gga agc ttg aag ctg tcg tct atg ttg ctg gag aca acc tca gga     1116
92   Glu Gly Ser Leu Lys Leu Ser Ser Met Leu Leu Glu Thr Thr Ser Gly
93           340                 345                 350
94   gca ctc tcc ctc tga ggggtcttct ctgaggtgca tggttctttt ggaagaaatg     1171
95   Ala Leu Ser Leu  *
96       355
97   agaaatacat gaaacagttt ccccactgat gggaccagag agagtgaaag agaaaagaaa   1231
98   actcagaaag ggatgaatct gaactatatg attacttgta gtcagaattt gccaaagcaa   1291
99   atatttcaaa atcaactgac tagtgcagga ggctgttgat tggctcttga ctgtgatgcc   1351
100   cgcaattctc aaaggaggac taaggaccgg cactgtggag caccctggct ttgccactcg   1411
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101        ccggagcatc aatgccgctg cctctggagg agcccttgga ttttctccat gcactgtgaa   1471
102        cttctgtggc ttcagttctc atgctgcctc ttccaaaagg ggacacagaa gcactggctg   1531
103        ctgctacaga ccgcaaaagc agaaagtttc gtgaaaatgt ccatctttgg gaaattttct   1591
104        accctgctct tgagcctgat aacccatgcc aggtcttata gattcctgat ctagaacctt   1651
105        tccaggcaat ctcagaccta atttccttct gttctccttg ttctgttctg ggccagtgaa   1711
106        ggtccttgtt ctgattttga aacgatctgc aggtcttgcc agtgaacccc tggacaactg   1771
107        accacaccca caaggcatcc aaagtctgtt ggcttccaat ccatttctgt gtcctgctgg   1831
108        aggttttaac ctagacaagg attccgctta ttccttggta tggtgacagt gtctctccat   1891
109        ggcctgagca gggagattat aacagctggg ttcgcaggag ccagccttgg ccctgttgta   1951
110        ggcttgttct gttgagtggc acttgctttg ggtccaccgt ctgtctgctc cctagaaaat   2011
111        gggctggttc ttttggccct cttctttctg aggcccactt tattctgagg aatacagtga   2071
112        gcagatatgg gcagcagcca ggtagggcaa aggggtgaag cgcaggcctt gctggaaggc   2131
113        tatttacttc catgcttctc cttttcttac tctatagtgg caacatttta aaagctttta   2191
114        acttagagat taggctgaaa aaaataagta atggaattca cctttgcatc ttttgtgtct   2251
115        ttcttatcat gatttggcaa aatgcatcac ctttgaaaat atttcacata ttggaaaagt   2311
116        gctttttaat gtgtatatga agcattaatt acttgtcact ttctttaccc tgtctcaata   2371
117        ttttaagtgt gtgcaattaa agatcaaata gatacattaa gagtgtgaag gctggtctga   2431
118        aggtagtgag ctatctcaat cggattgttc acactcagtt acagattgaa ctccttgttc   2491
119        tacttccctg cttctctcta ctgcaattga ctagtcttta aaaaaaagtg tgaagagtaa   2551
120        gcaataggga taaggaaata agatct                                       2577
122 <210> SEQ ID NO: 2
123 <211> LENGTH: 357
124 <212> TYPE: PRT
125 <213> ORGANISM: Homo sapiens
126 <400> SEQUENCE: 2
127        Met Ala Asp Asp Tyr Gly Ser Glu Ser Thr Ser Ser Met Glu Asp Tyr
128         1               5                  10                  15
129        Val Asn Phe Asn Phe Thr Asp Phe Tyr Cys Glu Lys Asn Asn Val Arg
130                    20                  25                  30
131        Gln Phe Ala Ser His Phe Leu Pro Pro Leu Tyr Trp Leu Val Phe Ile
132                35                  40                  45
133        Val Gly Ala Leu Gly Asn Ser Leu Val Ile Leu Val Tyr Trp Tyr Cys
134            50                  55                  60
135        Thr Arg Val Lys Thr Met Thr Asp Met Phe Leu Leu Asn Leu Ala Ile
136        65                  70                  75                  80
137        Ala Asp Leu Leu Phe Leu Val Thr Leu Pro Phe Trp Ala Ile Ala Ala
138                        85                  90                  95
139        Ala Asp Gln Trp Lys Phe Gln Thr Phe Met Cys Lys Val Val Asn Ser
140                    100                 105                 110
141        Met Tyr Lys Met Asn Phe Tyr Ser Cys Val Leu Leu Ile Met Cys Ile
142                115                 120                 125
143        Ser Val Asp Arg Tyr Ile Ala Ile Ala Gln Ala Met Arg Ala His Thr
144            130                 135                 140
145        Trp Arg Glu Lys Arg Leu Leu Tyr Ser Lys Met Val Cys Phe Thr Ile
146        145                 150                 155                 160
147        Trp Val Leu Ala Ala Ala Leu Cys Ile Pro Glu Ile Leu Tyr Ser Gln
148                        165                 170                 175
149        Ile Lys Glu Glu Ser Gly Ile Ala Ile Cys Thr Met Val Tyr Pro Ser
150                    180                 185                 190
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151        Asp Glu Ser Thr Lys Leu Lys Ser Ala Val Leu Thr Leu Lys Val Ile
152                195                 200                 205
153        Leu Gly Phe Phe Leu Pro Phe Val Val Met Ala Cys Cys Tyr Thr Ile
154            210                 215                 220
155        Ile Ile His Thr Leu Ile Gln Ala Lys Lys Ser Ser Lys His Lys Ala
156        225                 230                 235                 240
157        Leu Lys Val Thr Ile Thr Val Leu Thr Val Phe Val Leu Ser Gln Phe
158                        245                 250                 255
159        Pro Tyr Asn Cys Ile Leu Leu Val Gln Thr Ile Asp Ala Tyr Ala Met
160                    260                 265                 270
161        Phe Ile Ser Asn Cys Ala Val Ser Thr Asn Ile Asp Ile Cys Phe Gln
162                275                 280                 285
163        Val Thr Gln Thr Ile Ala Phe Phe His Ser Cys Leu Asn Pro Val Leu
164            290                 295                 300
165        Tyr Val Phe Val Gly Glu Arg Phe Arg Arg Asp Leu Val Lys Thr Leu
166        305                 310                 315                 320
167        Lys Asn Leu Gly Cys Ile Ser Gln Ala Gln Trp Val Ser Phe Thr Arg
168                        325                 330                 335
169        Arg Glu Gly Ser Leu Lys Leu Ser Ser Met Leu Leu Glu Thr Thr Ser
170                    340                 345                 350
171        Gly Ala Leu Ser Leu
172                355
174 <210> SEQ ID NO: 3
175 <211> LENGTH: 26
176 <212> TYPE: PRT
177 <213> ORGANISM: Artificial Sequence
178 <220> FEATURE:
179 <223> OTHER INFORMATION: NH2-Terminal Peptide of Human GPR-9-6
180 <400> SEQUENCE: 3
181        Met Ala Asp Asp Tyr Gly Ser Glu Ser Thr Ser Ser Met Glu Asp Tyr
182         1               5                  10                  15
183        Val Asn Phe Asn Phe Thr Asp Phe Tyr Cys
184                    20                  25
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187 <211> LENGTH: 35
188 <212> TYPE: DNA
189 <213> ORGANISM: Artificial Sequence
190 <220> FEATURE:
191 <223> OTHER INFORMATION: Oligonucleotide primer
192 <400> SEQUENCE: 4
193        tcgaagggat ccctaacatg gctgatgact atggc                              35
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196 <211> LENGTH: 35
197 <212> TYPE: DNA
198 <213> ORGANISM: Artificial Sequence
199 <220> FEATURE:
200 <223> OTHER INFORMATION: Oligonucleotide primer
201 <400> SEQUENCE: 5
202        aagaagtcta gaacccctca gagggagagt gctcc                              35
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Input Set : N:\Crf3\RULE60\09966755.raw
Output Set: N:\CRF3\01152002\I966755.raw

<210> SEQ ID NO: 6
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<210> SEQ ID NO: 7
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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VERIFICATION SUMMARY DATE: 01/15/2002
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